RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH
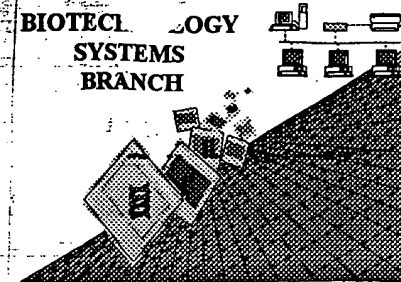
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/728,420_

Source: _OIPE_

Date Processed by STIC: _12/14/2000_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> SUGGESTED CORRECTION   SERIAL NUMBER: _09/728,420_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)   Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)   Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

OIPE

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     RAW SEQUENCE LISTING              DATE: 12/14/2000
     PATENT APPLICATION: US/09/728,420  TIME: 10:43:36

     Input Set : A:\A-579-c.app
     Output Set: N:\CRF3\12142000\I728420.raw

 3  <110> APPLICANT: Yoshinaga, Steven K.
 5  <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES INVOLVED IN IMMUNE RESPONSE
 7  <130> FILE REFERENCE: A-579-C
 9  <140> CURRENT APPLICATION NUMBER: US/09/728,420
10  <141> CURRENT FILING DATE: 2000-11-28
12  <160> NUMBER OF SEQ ID NOS: 35
14  <170> SOFTWARE: PatentIn Ver. 2.1
16  <210> SEQ ID NO: 1
17  <211> LENGTH: 600
18  <212> TYPE: DNA
19  <213> ORGANISM: mouse
21  <220> FEATURE:
22  <221> NAME/KEY: CDS
23  <222> LOCATION: Complement((1)..(600))
25  <400> SEQUENCE: 1
26  atg aag ccg tac ttc tgc cgt gtc ttt gtc ttc tgc ttc cta atc aga   48
27  Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
28   1               5                  10                  15
30  ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca   96
31  Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
32                  20                  25                  30
34  ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc  144
35  Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
36              35                  40                  45
38  cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa  192
39  Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
40          50                  55                  60
42  ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca  240
43  Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
44   65                  70                  75                  80
46  atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta  288
47  Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
48              85                  90                  95
50  aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc  336
51  Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
52              100                 105                 110
54  att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat  384
55  Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
56          115                 120                 125
58  ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta  432
59  Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
60          130                 135                 140
62  ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata  480
63  Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
64  145                 150                 155                 160
66  ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac  528
67  Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
```

```
68                  165                170              175
70 cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag    576
71 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
72          180                185              190
74 tct aga ctt gca ggt gtg acc tca                                    600
75 Ser Arg Leu Ala Gly Val Thr Ser
76          195                200
79 <210> SEQ ID NO: 2
80 <211> LENGTH: 200
81 <212> TYPE: PRT
82 <213> ORGANISM: mouse
84 <400> SEQUENCE: 2
85 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
86  1               5                10              15
88 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
89          20                25              30
91 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
92          35                40              45
94 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
95      50                55              60
97 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
98  65                70                75              80
100 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
101             85                90              95
103 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
104         100                105              110
106 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
107         115                120              125
109 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
110         130                135              140
112 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
113 145                150                155              160
115 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
116             165                170              175
118 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
119         180                185              190
121 Ser Arg Leu Ala Gly Val Thr Ser
122         195                200
126 <210> SEQ ID NO: 3
127 <211> LENGTH: 200
128 <212> TYPE: PRT
129 <213> ORGANISM: mouse
131 <400> SEQUENCE: 3
132 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
133  1               5                10              15
135 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
136             20                25              30
138 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
139         35                40              45
```

12/14/00

```
141 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
142     50                  55                  60
144 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
145 65                  70                  75                  80
147 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
148                 85                  90                  95
150 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
151                 100                 105                 110
153 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
154         115                 120                 125
156 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
157     130                 135                 140
159 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
160 145                 150                 155                 160
162 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
163                 165                 170                 175
165 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
166                 180                 185                 190
168 Ser Arg Leu Ala Gly Val Thr Ser
169         195                 200
172 <210> SEQ ID NO: 4
173 <211> LENGTH: 218
174 <212> TYPE: PRT
175 <213> ORGANISM: mouse
177 <400> SEQUENCE: 4
178 Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln
179  1                   5                  10                  15
181 Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val
182             20                  25                  30
184 Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
185         35                  40                  45
187 Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
188     50                  55                  60
190 Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
191 65                  70                  75                  80
193 Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
194                 85                  90                  95
196 Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
197                 100                 105                 110
199 Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
200         115                 120                 125
202 Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
203     130                 135                 140
205 Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
206 145                 150                 155                 160
208 Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
209                 165                 170                 175
211 Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
212             180                 185                 190
```

RAW SEQUENCE LISTING   DATE: 12/14/2000
PATENT APPLICATION: US/09/728,420   TIME: 10:43:36

Input Set : A:\A-579-c.app
Output Set: N:\CRF3\12142000\I728420.raw

```
214 Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
215       195             200             205
217 Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
218       210             215
221 <210> SEQ ID NO: 5
222 <211> LENGTH: 234
223 <212> TYPE: PRT
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Description of Artificial Sequence Synthetic
228       Oglionucleotide
230 <400> SEQUENCE: 5
```

This is an amino acid sequence.

```
W--> 231 Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg
232     1             5             10             15
W--> 234 Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
235             20             25             30
W--> 237 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
238             35             40             45
W--> 240 Val Xaa Xaa Ser Cys Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
241         50             55             60
W--> 243 Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Cys Xaa
244     65             70             75             80
W--> 246 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
247             85             90             95
W--> 249 Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Val Xaa Phe Xaa Leu
250             100             105             110
W--> 252 Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Phe Cys Xaa Xaa Xaa
253             115             120             125
W--> 255 Xaa Xaa Xaa Pro Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Gly Xaa
256     130             135             140
W--> 258 Xaa Xaa His Ile Xaa Glu Xaa Xaa Leu Cys Xaa Xaa Xaa Xaa Xaa Xaa
259     145             150             155             160
W--> 261 Lys Leu Xaa Trp Xaa Leu Xaa Val Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa
262             165             170             175
W--> 264 Xaa Xaa Leu Leu Xaa Xaa Xaa Xaa Leu Xaa Xaa Ile Trp Xaa Xaa Xaa
265             180             185             190
W--> 267 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa
268             195             200             205
W--> 270 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg
271             210             215             220
W--> 273 Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa
274     225             230
277 <210> SEQ ID NO: 6
278 <211> LENGTH: 966
279 <212> TYPE: DNA
280 <213> ORGANISM: mouse
282 <220> FEATURE:
283 <221> NAME/KEY: CDS
W--> 284 <222> LOCATION: Complement((1)..(966))
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see item 10 on Error Summary Sheet

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286 <400> SEQUENCE: 6
287 atg cag cta aag tgt ccc tgt ttt gtg tcc ttg gga acc agg cag cct    48
288 Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro
289   1               5                  10                  15
291 gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt    96
292 Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
293              20                  25                  30
295 ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act   144
296 Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
297           35                  40                  45
299 gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac   192
300 Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
301        50                  55                  60
303 ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa   240
304 Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
305  65                  70                  75                  80
307 atc gaa aac cca gaa gtt tcg gtg act tac tac ctg cct tac aag tct   288
308 Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
309              85                  90                  95
311 cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc   336
312 Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
313             100                 105                 110
315 ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc   384
316 Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
317            115                 120                 125
319 acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca   432
320 Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
321        130                 135                 140
323 gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg   480
324 Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
325 145                 150                 155                 160
327 gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac   528
328 Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
329             165                 170                 175
331 ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca   576
332 Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
333             180                 185                 190
335 gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac   624
336 Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
337             195                 200                 205
339 acg gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat   672
340 Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
341        210                 215                 220
343 gat gta atc agc aca tta agg ctc cct tgg aca tct cgt ggg gat gtt   720
344 Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
345 225                 230                 235                 240
347 ctg tgc tgc gta gag aat gtg gct ctc cac cag aac atc act agc att   768
348 Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
349             245                 250                 255
```

FYI:

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 12/14/2000
PATENT APPLICATION: US/09/728,420   TIME: 10:43:37

Input Set : A:\A-579-c.app
Output Set: N:\CRF3\12142000\I728420.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:23 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:1, CDS LOCATION: Complement((1)..(600))
L:231 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:231 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:231 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:234 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:234 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:237 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:237 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:240 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:240 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:243 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:243 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:246 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:246 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:249 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:249 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:252 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:258 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:258 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:261 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:261 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:264 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:264 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:267 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:267 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:273 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:273 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:284 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:6, CDS LOCATION: Complement((1)..(966))
L:589 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:589 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:589 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
L:592 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:592 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:595 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:595 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:598 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:598 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:601 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:601 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10

VERIFICATION SUMMARY   DATE: 12/14/2000
PATENT APPLICATION: US/09/728,420 TIME: 10:43:37

Input Set : A:\A-579-c.app
Output Set: N:\CRF3\12142000\I728420.raw

```
L:604 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:604 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:607 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:607 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:610 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:610 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:613 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:613 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:616 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:616 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:660 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:11, CDS LOCATION: Complement((1)..(864))
L:927 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:1298 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
M:340 Repeated in SeqNo=20
```